What is claimed is:

1. (Original) An isolated biomarker comprising two or more genes selected from the group consisting of the 31 genes as set out in Tables 2 and 3.

2. (Original) The isolated biomarker of claim 1 consisting essentially of the 31 genes as set out in Tables 2 and 3.

3. (Original) An isolated biomarker comprising one or more polynucleotide sequences from the 5' region of a gene selected from the group consisting of the 31 genes as set out in Tables 2 and 3.

4. (Original) An isolated biomarker comprising one or more polynucleotide sequences from the 3' region of a gene selected from the group consisting of the genes as set out in Tables 2 and 3.

5. (Original) An isolated biomarker comprising one or more polynucleotide sequences from the internal coding region of a gene selected from the group consisting of the 31 genes as set out in Tables 2 and 3.

6. (Original) An isolated biomarker comprising the polypeptide sequences encoded by two or more genes selected from the group consisting of the 31 genes as set out in Tables 2 and 3.

7. (Original) The isolated biomarker of claim 6 consisting essentially of the polypeptide sequences encoded by the 31 genes, as set out in Tables 2 and 3.

8. (Original) An isolated biomarker comprising the amino terminal polypeptide sequences encoded by one or more polynucleotide sequences from the 5' region of a gene selected from the group consisting of the 31 genes as set out in Tables 2 and 3.

9. (Original) An isolated biomarker comprising the carboxy terminal polypeptide sequences encoded by one or more polynucleotide sequences from the 3' region of a gene selected from the group consisting of the 31 genes as set out in Tables 2 and 3.

10. (Original) An isolated biomarker comprising the internal polypeptide sequences encoded by one or more polynucleotide sequences from the internal coding region of a gene selected from the group consisting of the 31 genes as set out in Tables 2 and 3.

11. (Currently amended) A method of identifying an inhibitor of ~~B2M~~ an activity of beta2-microglobulin, said method comprising ~~the steps of~~:

a) contacting chondrocytes with ~~B2M~~ beta2-microglobulin in ~~the~~ a presence of a candidate modulator and in an absence of ~~a~~ said candidate modulator; and

b) comparing the proliferation of said chondrocytes in ~~the~~ said presence relative to ~~the~~ said absence of said candidate modulator, wherein ~~an~~ a specific increase in the proliferation of said chondrocytes in ~~the~~ said presence relative to ~~the~~ said absence of said candidate modulator identifies said candidate modulator as ~~an~~ said inhibitor of ~~B2M~~ said activity of said-beta2-microglobulin.

12. (Original) A method of identifying an inhibitor of B2M activity said method comprising the steps of:

a) contacting chondrocytes with B2M in the presence and absence of a candidate modulator, and

b) comparing the level of differential expression of a biomarker comprising one or more polynucleotide sequences of one or more genes selected from the group consisting of the 31 genes as set out in Tables 2 and 3 in the presence relative to the absence of said candidate modulator, wherein differentially decreased expression of said biomarker identifies said candidate modulator as an inhibitor of B2M activity.

13. (Original) The method of claim 12, wherein said polynucleotide sequences are from the 5' region of a gene selected from the group consisting of the 31 genes as set out in Tables 2 and 3.

14. (Original) The method of claim 12, wherein said polynucleotide sequences are from the 3' region of a gene selected from the group consisting of the 31 genes as set out in Tables 2 and 3.

15. (Original) The method of claim 12, wherein said polynucleotide sequences are from the internal coding region of a gene selected from the group consisting of the 31 genes as set out in Tables 2 and 3.

16. (Original) A method of identifying an inhibitor of B2M activity said method comprising the steps of:

a) contacting chondrocytes with B2M in the presence and absence of a candidate modulator, and

b) comparing the level of differential expression of a biomarker comprising one or more polypeptide sequences of one or more genes selected from the group consisting of the 31 genes as set out in Tables 2 and 3 in the presence relative to the absence of said candidate modulator, wherein differentially increased expression of said biomarker identifies said candidate modulator as an inhibitor of B2M or B2M related activity.

17. (Original) The method of claim 16, said polypeptide sequences are amino terminal polypeptide sequences encoded by one or more polynucleotide sequences from the 5' region of a gene selected from the group consisting of the 31 genes as set out in Tables 2 and 3.

18. (Original) The method of claim 16, said polypeptide sequences are carboxy terminal polypeptide sequences encoded by one or more polynucleotide sequences from the 3' region of a gene selected from the group consisting of the 31 genes as set out in Tables 2 and 3.

19. (Original) The method of claim 16, said polypeptide sequences are internal polypeptide sequences encoded by one or more polynucleotide sequences from the internal coding region of a gene selected from the group consisting of the 31 genes as set out in Tables 2 and 3.

20. (New) The method of claim 11, wherein said chondrocytes are derived from a subject having osteoarthritis.

21. (New) The method of claim 11, wherein said chondrocytes are derived from a subject having severe osteoarthritis.

22. (New) The method of claim 11, wherein said chondrocytes are primary chondrocytes.

23. (New) The method of claim 11, wherein said chondrocytes are cultured chondrocytes.

24. (New) The method of claim 11, wherein said chondrocytes are human chondrocytes.